SEQUENCE LISTING

<110> Svendsen, Allan
Kjaerulff, Soren
Bisgard-Frantzen, Henrik
Andersen, Carsten

<120> Alpha-amylase variants

<130> 5709.200-US

<160> 31

<170> PatentIn version 3.1

<210> 1
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 1

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His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1               5                  10                  15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
            20                  25                  30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
        35                  40                  45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
    50                  55                  60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65                  70                  75                  80

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
                85                  90                  95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
        115                 120                 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
    130                 135                 140
```

```
Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145                 150                 155                 160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
                165                 170                 175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
            180                 185                 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
        195                 200                 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
    210                 215                 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225                 230                 235                 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
                245                 250                 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
            260                 265                 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
        275                 280                 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
    290                 295                 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305                 310                 315                 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
                325                 330                 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
            340                 345                 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365
```

C1 Cont

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Val Trp Val Lys Gln
485

<210> 2
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 2

C1 Cont

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
85 90 95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
210 215 220

C1
Cont

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
450 455 460

C' Cont

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Lys Arg
485

<210> 3
<211> 514
<212> PRT
<213> Bacillus stearothermophilus

<400> 3

Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu

```
1               5                   10                  15

Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
            20                  25                  30

Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
        35                  40                  45

Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
    50                  55                  60

Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr
65                  70                  75                  80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
                85                  90                  95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
            100                 105                 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
        115                 120                 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
    130                 135                 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
145                 150                 155                 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
                165                 170                 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
            180                 185                 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
        195                 200                 205

Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn
    210                 215                 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
225                 230                 235                 240
```

C1 Cont

Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly
245 250 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
260 265 270

Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp
275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr
290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
385 390 395 400

C1
Cont

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val
405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr
485 490 495

Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
500 505 510

Ala Trp

<210> 4
<211> 483
<212> PRT
<213> Bacillus licheniformis

<400> 4

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro

```
    130                 135                 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145                 150                 155                 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
                165                 170                 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
            180                 185                 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
        195                 200                 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
    210                 215                 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
                245                 250                 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
            260                 265                 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
        275                 280                 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
    290                 295                 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305                 310                 315                 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325                 330                 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                 345                 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                 360                 365
```

C' Cont.

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Arg

<210> 5
<211> 480
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 5

C1 Cont

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
1 5 10 15

Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60

```
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65                  70                  75                  80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85                  90                  95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115                 120                 125

Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
    130                 135                 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
            180                 185                 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
        195                 200                 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
    210                 215                 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
                245                 250                 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
            260                 265                 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
        275                 280                 285

His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
```

C1 Cont.

```
    290                 295                 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325                 330                 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                 345                 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                 360                 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
    370                 375                 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385                 390                 395                 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
        435                 440                 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
    450                 455                 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465                 470                 475                 480
```

C' cont.

<210> 6
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 6

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His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1               5                   10                  15
```

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg
165 170 175

C1 Cont

Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

C1 Cont

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser

465 470 475 480

Ile Trp Val Asn Lys
485

<210> 7
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 7

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

C1 cont.

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
115 120 125

Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
165 170 175

```
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
            180                 185                 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
        195                 200                 205

Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
    210                 215                 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225                 230                 235                 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
                245                 250                 255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
            260                 265                 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
        275                 280                 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
    290                 295                 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305                 310                 315                 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
                325                 330                 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
            340                 345                 350

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
    370                 375                 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385                 390                 395                 400
```

C1 Cont

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Val Trp Val Lys Gln
485

<210> 8
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 8

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
20 25 30

Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
35 40 45

C1 Cont.

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
85 90 95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
210 215 220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
245 250 255

Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

C1 Cont.

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

```
Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
            340                 345                 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
    370                 375                 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
385                 390                 395                 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
                405                 410                 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
            420                 425                 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
        435                 440                 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
    450                 455                 460

Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465                 470                 475                 480

Ile Trp Val Lys Arg
                485
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<210> 9
<211> 1455
<212> DNA
<213> Bacillus sp.

<400> 9
catcataatg gaacaaatgg tactatgatg caatatttcg aatggtattt gccaaatgac 60

gggaatcatt ggaacaggtt gagggatgac gcagctaact taaagagtaa agggataaca 120

gctgtatgga tcccacctgc atggaagggg acttcccaga atgatgtagg ttatggagcc 180

tatgatttat atgatcttgg agagtttaac cagaagggga cggttcgtac aaaatatgga 240

acacgcaacc agctacaggc tgcggtgacc tctttaaaaa ataacggcat tcaggtatat 300

ggtgatgtcg tcatgaatca taaaggtgga gcagatggta cggaaattgt aaatgcggta 360

gaagtgaatc ggagcaaccg aaaccaggaa acctcaggag agtatgcaat agaagcgtgg 420

acaaagtttg attttcctgg aagaggaaat aaccattcca gctttaagtg gcgctggtat 480

cattttgatg ggacagattg ggatcagtca cgccagcttc aaaacaaaat atataaattc 540

aggggaacag gcaaggcctg ggactgggaa gtcgatacag agaatggcaa ctatgactat 600

cttatgtatg cagacgtgga tatggatcac ccagaagtaa tacatgaact tagaaactgg 660

ggagtgtggt atacgaatac actgaacctt gatggattta gaatagatgc agtgaaacat 720

ataaaatata gctttacgag agattggctt acacatgtgc gtaacaccac aggtaaacca 780

atgtttgcag tggctgagtt ttggaaaaat gaccttggtg caattgaaaa ctatttgaat 840

aaaacaagtt ggaatcactc ggtgtttgat gttcctctcc actataattt gtacaatgca 900

tctaatagcg gtggttatta tgatatgaga aatattttaa atggttctgt ggtgcaaaaa 960

catccaacac atgccgttac ttttgttgat aaccatgatt ctcagcccgg ggaagcattg 1020

gaatcctttg ttcaacaatg gtttaaacca cttgcatatg cattggttct gacaagggaa 1080

caaggttatc cttccgtatt ttatggggat tactacggta tcccaaccca tggtgttccg 1140

gctatgaaat ctaaaataga ccctcttctg caggcacgtc aaacttttgc ctatggtacg 1200

cagcatgatt actttgatca tcatgatatt atcggttgga caagagaggg aaatagctcc 1260

catccaaatt caggccttgc caccattatg tcagatggtc caggtggtaa caaatggatg 1320

tatgtgggga aaaataaagc gggacaagtt tggagagata ttaccggaaa taggacaggc 1380

accgtcacaa ttaatgcaga cggatggggt aatttctctg ttaatggagg gtccgtttcg 1440

gtttgggtga agcaa 1455

<210> 10
<211> 1455
<212> DNA
<213> Bacillus sp.

<400> 10
catcataatg ggacaaatgg gacgatgatg caatactttg aatggcactt gcctaatgat 60

gggaatcact ggaatagatt aagagatgat gctagtaatc taagaaatag aggtataacc 120

gctatttgga ttccgcctgc ctggaaaggg acttcgcaaa atgatgtggg gtatggagcc 180

tatgatcttt atgatttagg ggaatttaat caaaagggga cggttcgtac taagtatggg 240

acacgtagtc aattggagtc tgccatccat gctttaaaga ataatggcgt tcaagtttat 300

ggggatgtag tgatgaacca taaaggagga gctgatgcta cagaaaacgt tcttgctgtc 360

gaggtgaatc caaataaccg gaatcaagaa atatctgggg actacacaat tgaggcttgg 420

actaagtttg attttccagg gaggggtaat acatactcag actttaaatg gcgttggtat 480

catttcgatg gtgtagattg ggatcaatca cgacaattcc aaaatcgtat ctacaaattc 540

cgaggtgatg gtaaggcatg ggattgggaa gtagattcgg aaaatggaaa ttatgattat 600

ttaatgtatg cagatgtaga tatggatcat ccggaggtag taaatgagct tagaagatgg 660

ggagaatggt atacaaatac attaaatctt gatggattta ggatcgatgc ggtgaagcat 720

attaaatata gctttacacg tgattggttg acccatgtaa gaaacgcaac gggaaaagaa 780

atgtttgctg ttgctgaatt ttggaaaaat gatttaggtg ccttggagaa ctatttaaat 840

aaaacaaact ggaatcattc tgtctttgat gtccccttc attataatct ttataacgcg 900

tcaaatagtg gaggcaacta tgacatggca aaacttctta atggaacggt tgttcaaaag 960

catccaatgc atgccgtaac ttttgtggat aatcacgatt ctcaacctgg ggaatcatta 1020

gaatcatttg tacaagaatg gtttaagcca cttgcttatg cgcttatttt aacaagagaa 1080

caaggctatc cctctgtctt ctatggtgac tactatggaa ttccaacaca tagtgtccca 1140

gcaatgaaag ccaagattga tccaatctta gaggcgcgtc aaaattttgc atatggaaca 1200

caacatgatt attttgacca tcataatata atcggatgga cacgtgaagg aaataccacg 1260

catcccaatt caggacttgc gactatcatg tcggatgggc caggggggaga gaaatggatg 1320

tacgtagggc aaaataaagc aggtcaagtt tggcatgaca taactggaaa taaaccagga 1380

acagttacga tcaatgcaga tggatgggct aatttttcag taaatggagg atctgtttcc 1440

atttgggtga aacga 1455

<210> 11
<211> 1548
<212> DNA
<213> Bacillus stearothermophilus

C1 Cont

<400> 11
gccgcaccgt ttaacggcac catgatgcag tattttgaat ggtacttgcc ggatgatggc 60

acgttatgga ccaaagtggc caatgaagcc aacaacttat ccagccttgg catcaccgct 120

ctttggctgc cgcccgctta caaaggaaca agccgcagcg acgtagggta cggagtatac 180

gacttgtatg acctcggcga attcaatcaa aaagggaccg tccgcacaaa atacggaaca 240

aaagctcaat atcttcaagc cattcaagcc gcccacgccg ctggaatgca agtgtacgcc 300

gatgtcgtgt tcgaccataa aggcggcgct gacggcacgg aatgggtgga cgccgtcgaa 360

gtcaatccgt ccgaccgcaa ccaagaaatc tcgggcacct atcaaatcca agcatggacg 420

aaatttgatt ttcccgggcg gggcaacacc tactccagct ttaagtggcg ctggtaccat 480

tttgacggcg ttgattggga cgaaagccga aaattgagcc gcatttacaa attccgcggc 540

atcggcaaag cgtgggattg ggaagtagac acggaaaacg gaaactatga ctacttaatg 600

tatgccgacc ttgatatgga tcatcccgaa gtcgtgaccg agctgaaaaa ctgggggaaa 660

tggtatgtca acacaacgaa cattgatggg ttccggcttg atgccgtcaa gcatattaag 720

ttcagttttt ttcctgattg gttgtcgtat gtgcgttctc agactggcaa gccgctattt 780

accgtcgggg aatattggag ctatgacatc aacaagttgc acaattacat tacgaaaaca 840

gacggaacga tgtctttgtt tgatgccccg ttacacaaca aattttatac cgcttccaaa 900

tcaggggcg catttgatat gcgcacgtta atgaccaata ctctcatgaa agatcaaccg 960

acattggccg tcaccttcgt tgataatcat gacaccgaac ccggccaagc gctgcagtca 1020

tgggtcgacc catggttcaa accgttggct tacgccttta ttctaactcg gcaggaagga 1080

tacccgtgcg tcttttatgg tgactattat ggcattccac aatataacat tccttcgctg 1140

aaaagcaaaa tcgatccgct cctcatcgcg cgcagggatt atgcttacgg aacgcaacat 1200

gattatcttg atcactccga catcatcggg tggacaaggg aaggggcac tgaaaaacca 1260

ggatccggac tggccgcact gatcaccgat gggccgggag gaagcaaatg gatgtacgtt 1320

ggcaaacaac acgctggaaa agtgttctat gaccttaccg gcaaccggag tgacaccgtc 1380

accatcaaca gtgatggatg gggggaattc aaagtcaatg gcggttcggt ttcggtttgg 1440

gttcctagaa aaacgaccgt ttctaccatc gctcggccga tcacaacccg accgtggact 1500

ggtgaattcg tccgttggac cgaaccacgg ttggtggcat ggccttga 1548

C1
Cont.

<210> 12
<211> 1920
<212> DNA
<213> Bacillus licheniformis

<220>
<221> misc_feature
<222> (421)..(1872)
<223> CDS

<400> 12
cggaagattg gaagtacaaa aataagcaaa agattgtcaa tcatgtcatg agccatgcgg 60

gagacggaaa aatcgtctta atgcacgata tttatgcaac gttcgcagat gctgctgaag 120

agattattaa aaagctgaaa gcaaaaggct atcaattggt aactgtatct cagcttgaag 180

aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatatc ggcgcttttc 240

ttttggaaga aaatataggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca 300

tcatatgttt cacattgaaa ggggaggaga atcatgaaac aacaaaaacg gctttacgcc 360

cgattgctga cgctgttatt tgcgctcatc ttcttgctgc ctcattctgc agcagcggcg 420

gcaaatctta atgggacgct gatgcagtat tttgaatggt acatgcccaa tgacggccaa 480

cattggaggc gtttgcaaaa cgactcggca tatttggctg aacacggtat tactgccgtc 540

tggattcccc cggcatataa gggaacgagc caagcggatg tgggctacgg tgcttacgac 600

ctttatgatt taggggagtt tcatcaaaaa gggacggttc ggacaaagta cggcacaaaa 660

ggagagctgc aatctgcgat caaaagtctt cattcccgcg acattaacgt ttacggggat 720

gtggtcatca accacaaagg cggcgctgat gcgaccgaag atgtaaccgc ggttgaagtc 780

gatcccgctg accgcaaccg cgtaatttca ggagaacacc taattaaagc ctggacacat 840

tttcattttc cggggcgcgg cagcacatac agcgatttta aatggcattg gtaccatttt 900

gacggaaccg attgggacga gtcccgaaag ctgaaccgca tctataagtt tcaaggaaag 960

gcttgggatt gggaagtttc caatgaaaac ggcaactatg attatttgat gtatgccgac 1020

atcgattatg accatcctga tgtcgcagca gaaattaaga gatggggcac ttggtatgcc 1080

aatgaactgc aattggacgg tttccgtctt gatgctgtca aacacattaa attttctttt 1140

ttgcgggatt gggttaatca tgtcagggaa aaaacgggga aggaaatgtt tacggtagct 1200

gaatattggc agaatgactt gggcgcgctg gaaaactatt tgaacaaaac aaattttaat 1260

cattcagtgt ttgacgtgcc gcttcattat cagttccatg ctgcatcgac acagggaggc 1320

ggctatgata tgaggaaatt gctgaacggt acggtcgttt ccaagcatcc gttgaaatcg 1380

gttacatttg tcgataacca tgatacacag ccggggcaat cgcttgagtc gactgtccaa 1440

acatggttta agccgcttgc ttacgctttt attctcacaa gggaatctgg ataccctcag 1500

gttttctacg gggatatgta cgggacgaaa ggagactccc agcgcgaaat tcctgccttg 1560

aaacacaaaa ttgaaccgat cttaaaagcg agaaaacagt atgcgtacgg agcacagcat 1620

gattatttcg accaccatga cattgtcggc tggacaaggg aaggcgacag ctcggttgca 1680

aattcaggtt tggcggcatt aataacagac ggacccggtg gggcaaagcg aatgtatgtc 1740

ggccggcaaa acgccggtga gacatggcat gacattaccg gaaaccgttc ggagccggtt 1800

C1 Cont.

gtcatcaatt cggaaggctg gggagagttt cacgtaaacg gcgggtcggt ttcaatttat 1860

gttcaaagat agaagagcag agaggacgga tttcctgaag gaaatccgtt tttttatttt 1920

<210> 13
<211> 1455
<212> DNA
<213> Bacillus sp.

<400> 13
catcataatg gaacaaatgg tactatgatg caatatttcg aatggtattt gccaaatgac 60

gggaatcatt ggaacaggtt gagggatgac gcagctaact taaagagtaa agggataaca 120

gctgtatgga tcccacctgc atggaagggg acttcccaga atgatgtagg ttatggagcc 180

tatgatttat atgatcttgg agagtttaac cagaagggga cggttcgtac aaaatatgga 240

acacgcaacc agctacaggc tgcggtgacc tctttaaaaa ataacggcat tcaggtatat 300

ggtgatgtcg tcatgaatca taaaggtgga gcagatggta cggaaattgt aaatgcggta 360

gaagtgaatc ggagcaaccg aaaccaggaa acctcaggag agtatgcaat agaagcgtgg 420

acaaagtttg attttcctgg aagaggaaat aaccattcca gctttaagtg gcgctggtat 480

cattttgatg ggacagattg ggatcagtca cgccagcttc aaaacaaaat atataaattc 540

aggggaacag gcaaggcctg ggactgggaa gtcgatacag agaatggcaa ctatgactat 600

cttatgtatg cagacgtgga tatggatcac ccagaagtaa tacatgaact tagaaactgg 660

ggagtgtggt atacgaatac actgaacctt gatggattta gaatagatgc agtgaaacat 720

ataaaatata gctttacgag agattggctt acacatgtgc gtaacaccac aggtaaacca 780

atgtttgcag tggctgagtt ttggaaaaat gaccttggtg caattgaaaa ctatttgaat 840

aaaacaagtt ggaatcactc ggtgtttgat gttcctctcc actataattt gtacaatgca 900

tctaatagcg gtggttatta tgatatgaga aatattttaa atggttctgt ggtgcaaaaa 960

C1 Cont
catccaacac atgccgttac ttttgttgat aaccatgatt ctcagcccgg ggaagcattg 1020

gaatcctttg ttcaacaatg gtttaaacca cttgcatatg cattggttct gacaagggaa 1080

caaggttatc cttccgtatt ttatggggat tactacggta tcccaaccca tggtgttccg 1140

gctatgaaat ctaaaataga ccctcttctg caggcacgtc aaacttttgc ctatggtacg 1200

cagcatgatt actttgatca tcatgatatt atcggttgga caagagaggg aaatagctcc 1260

catccaaatt caggccttgc caccattatg tcagatggtc caggtggtaa caaatggatg 1320

tatgtgggga aaaataaagc gggacaagtt tggagagata ttaccggaaa taggacaggc 1380

accgtcacaa ttaatgcaga cggatggggt aatttctctg ttaatggagg gtccgtttcg 1440

gtttgggtga agcaa 1455

<210> 14
<211> 1455
<212> DNA
<213> Bacillus sp.

<400> 14
catcataatg ggacaaatgg gacgatgatg caatactttg aatggcactt gcctaatgat 60

gggaatcact ggaatagatt aagagatgat gctagtaatc taagaaatag aggtataacc 120

gctatttgga ttccgcctgc ctggaaaggg acttcgcaaa atgatgtggg gtatggagcc 180

tatgatcttt atgatttagg ggaatttaat caaaagggga cggttcgtac taagtatggg 240

acacgtagtc aattggagtc tgccatccat gctttaaaga ataatggcgt tcaagtttat 300

ggggatgtag tgatgaacca taaaggagga gctgatgcta cagaaaacgt tcttgctgtc 360

gaggtgaatc caaataaccg gaatcaagaa atatctgggg actacacaat tgaggcttgg 420

actaagtttg attttccagg gaggggtaat acatactcag actttaaatg gcgttggtat 480

catttcgatg gtgtagattg ggatcaatca cgacaattcc aaaatcgtat ctacaaattc 540

cgaggtgatg gtaaggcatg ggattgggaa gtagattcgg aaaatggaaa ttatgattat 600

ttaatgtatg cagatgtaga tatggatcat ccggaggtag taaatgagct tagaagatgg 660

ggagaatggt atacaaatac attaaatctt gatggattta ggatcgatgc ggtgaagcat 720

attaaatata gctttacacg tgattggttg acccatgtaa gaaacgcaac gggaaaagaa 780

atgtttgctg ttgctgaatt ttggaaaaat gatttaggtg ccttggagaa ctatttaaat 840

aaaacaaact ggaatcattc tgtctttgat gtccccccttc attataatct ttataacgcg 900

tcaaatagtg gaggcaacta tgacatggca aaacttctta atggaacggt tgttcaaaag 960

catccaatgc atgccgtaac ttttgtggat aatcacgatt ctcaacctgg ggaatcatta 1020

gaatcatttg tacaagaatg gtttaagcca cttgcttatg cgcttatttt aacaagagaa 1080

caaggctatc cctctgtctt ctatggtgac tactatggaa ttccaacaca tagtgtccca 1140

gcaatgaaag ccaagattga tccaatctta gaggcgcgtc aaaattttgc atatggaaca 1200

caacatgatt attttgacca tcataatata atcggatgga cacgtgaagg aaataccacg 1260

catcccaatt caggacttgc gactatcatg tcggatgggc caggggggaga gaaatggatg 1320

tacgtagggc aaaataaagc aggtcaagtt tggcatgaca taactggaaa taaaccagga 1380

acagttacga tcaatgcaga tggatgggct aatttttcag taaatggagg atctgtttcc 1440

atttgggtga aacga 1455

<210> 15
<211> 74
<212> DNA
<213> Artificial sequence

<220>
<223> Primer RSERI

<220>
<221> misc_feature
<222> (21)..(62)
<223> The nucleotides in positions 21-62 were synthesized as: 312234322 2 4333313344
4233423242 2122112433 43, where 1:(97%A, 1%T, 1%C, 1%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%G, 1%A, 1%T, 1%C).

<400> 15
gcgttttgcc ggccgacata nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nncaaacctg aatt 74

<210> 16
<211> 122
<212> DNA
<213> Artificial sequence

<220>
<223> Primer RSERII

<220>
<221> misc_feature
<222> (63)..(104)
<223> The nucleotides in positions 73-114 were synthesized as: 31113324 1122243113 3414324234 3322333224 2331, where 1:(97%A, 1%T, 1%C, 1%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%G, 1%A, 1%T, 1%C).

C1 Cont

<400> 16
gcgttttgcc ggccgacata cattcgcttt gccccaccgg gtccgtctgt tattaatgcc 60

gcnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnngccgac aatgtcatgg 120

tg 122

<210> 17
<211> 78

<212> DNA
<213> Artificial sequence

<220>
<223> Primer RSERIII

<220>
<221> misc_feature
<222> (19)..(60)
<223> The nucleotides in positions 19-60 were synthesized as: 43 341311 2423 1244244234 1112112312 4324243233, where 1:(97%A, 1%T, 1%C, 1%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%G, 1%A, 1%T, 1%C).

<400> 17
gtcgccttcc cttgtccann nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

gtacgcatac tgttttct 78

<210> 18
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer FSERIII

<400> 18
tggacaaggg aaggcgacag 20

<210> 19
<211> 81
<212> DNA
<213> Artificial sequence

<220>
<223> Primer RSERV

<220>
<221> misc_feature
<222> (19)..(60)
<223> The nucleotides in positions 19-60 were synthesized as: 42 422231 1443 1441122234 3432444142 3233222342, where 1:(97%A, 1%T, 1%C, 1%G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97%G, 1%A, 1%T, 1%C).

C1 cont

<400> 19
taagatcggt tcaattttnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

cccgtacata tccccgtaga a 81

<210> 20

<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Primer FSERV

<400> 20
aaaattgaac cgatctta 18

<210> 21
<211> 107
<212> DNA
<213> Artificial sequence

<220>
<223> Primer FSERVII

<220>
<221> misc_feature
<222> (54)..(95)
<223> The nucleotides in positions 54-95 were synthesized as: 3442134 4 234222331 1431233422 4111234422 13122, where 1:(97%A, 1%T, 1%C, 1 %G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97% G, 1%A, 1%T, 1%C).

<400> 21
ttccatgctg catcgacaca gggaggcggc tatgatatga ggaaattgct gaannnnnnn 60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnntgtcg ataacca 107

<210> 22
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Primer RSERVII

<400> 22
tgtcgatgca gcatggaa 18

C1 Cont

<210> 23
<211> 80
<212> DNA
<213> Artificial sequence

<220>
<223> Primer FSERIX

<220>
<221> misc_feature
<222> (21)..(62)

<223> The nucleotides in positions 21-62 were synthesized as: 432243221 3 4322221223 2313114441 1232441213 33, where 1:(97%A, 1%T, 1%C, 1 %G); 2:(97%T, 1%A, 1%C, 1%G); 3:(97%C, 1%A, 1%T, 1%G); and 4:(97% G, 1%A, 1%T, 1%C).

<400> 23
gtccaaacat ggtttaagcc nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nntcaggttt tctacgggga 80

<210> 24
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer RSERIX

<400> 24
ggcttaaacc atgtttggac 20

<210> 25
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Primer 1B

<400> 25
cgattgctga cgctgttatt tgcg 24

<210> 26
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Primer #63

C! Cont

<400> 26
ctatctttga acataaattg aaacc 25

<210> 27
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Forward Primer1

<400> 27

gacctgcagt caggcaacta 20

<210> 28
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse Primer1

<400> 28
tagagtcgac ctgcaggcat 20

<210> 29
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Forward Primer2

<400> 29
gacctgcagt caggcaacta 20

<210> 30
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Reverse Primer2

<400> 30
tagagtcgac ctgcaggcat 20

<210> 31
<211> 2084
<212> DNA
<213> Bacillus amyloliquefaciens

<220>
<221> misc_feature
<222> (343)..(1794)
<223> CDS

C1 Cont

<400> 31
gccccgcaca tacgaaaaga ctggctgaaa acattgagcc tttgatgact gatgatttgg 60

ctgaagaagt ggatcgattg tttgagaaaa gaagaagacc ataaaaatac cttgtctgtc 120

atcagacagg gtatttttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa 180

gggggttgt tattatttta ctgatatgta aaatataatt tgtataagaa aatgagaggg 240

agaggaaaca tgattcaaaa acgaaagcgg acagtttcgt tcagacttgt gcttatgtgc 300

acgctgttat ttgtcagttt gccgattaca aaaacatcag ccgtaaatgg cacgctgatg 360

cagtattttg aatggtatac gccgaacgac ggccagcatt ggaaacgatt gcagaatgat 420

gcggaacatt tatcggatat cggaatcact gccgtctgga ttcctcccgc atacaaagga 480

ttgagccaat ccgataacgg atacggacct tatgatttgt atgatttagg agaattccag 540

caaaaaggga cggtcagaac gaaatacggc acaaaatcag agcttcaaga tgcgatcggc 600

tcactgcatt cccggaacgt ccaagtatac ggagatgtgg ttttgaatca taaggctggt 660

gctgatgcaa cagaagatgt aactgccgtc gaagtcaatc cggccaatag aaatcaggaa 720

acttcggagg aatatcaaat caaagcgtgg acggattttc gttttccggg ccgtggaaac 780

acgtacagtg attttaaatg gcattggtat catttcgacg gagcggactg ggatgaatcc 840

cggaagatca gccgcatctt taagtttcgt ggggaaggaa aagcgtggga ttgggaagta 900

tcaagtgaaa acggcaacta tgactattta atgtatgctg atgttgacta cgaccaccct 960

gatgtcgtgg cagagacaaa aaaatggggt atctggtatg cgaatgaact gtcattagac 1020

ggcttccgta ttgatgccgc caaacatatt aaattttcat ttctgcgtga ttgggttcag 1080

gcggtcagac aggcgacggg aaaagaaatg tttacggttg cggagtattg gcagaataat 1140

gccgggaaac tcgaaaacta cttgaataaa acaagcttta atcaatccgt gtttgatgtt 1200

ccgcttcatt tcaatttaca ggcggcttcc tcacaaggag gcggatatga tatgaggcgt 1260

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C1 Cont

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